

SEQUENCE LISTING

<110> Presnell, Scott R.
 Conklin, Darrell C.
 Novak, Julia E.
 Hammond, Angela K.

<120> POLYNUCLEOTIDES ENCODING CYTOKINE RECEPTOR ZALPHA11

<130> 98-55D2

<150> US 60/100,896

<151> 1998-09-23

<150> US 60/123,546

<151> 1999-03-09

<150> US 60/142,574

<151> 1999-07-06

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<213> Homo sapiens

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 cag gga ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc gat tac ctc	158
Gln Gly Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu	
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35 40 45	
ctc acc ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc Leu Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala	254
50 55 60	
acc tcc tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc Thr Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr	302
65 70 75	
tac acc tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc Tyr Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe	350
80 85 90	
agt gtc aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc Ser Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly	398
95 100 105 110	
agc ttt ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg Ser Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val	446
115 120 125	
act gtg acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac Thr Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr	494
130 135 140	
gaa gac cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg Glu Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu	542
145 150 155	
cag tac agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag Gln Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys	590
160 165 170	
ctg atc tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc Leu Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe	638
175 180 185 190	
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Gly Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile			
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ttt cag acc cag tca gag gag tta aag gaa ggc tgg aac cct cac ctg			782
Phe Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu			
225	230	235	
ctg ctt ctc ctc ctg ctt gtc ata gtc ttc att cct gcc ttc tgg agc			830
Leu Leu Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser			
240	245	250	
ctg aag acc cat cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc			878
Leu Lys Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val			
255	260	265	270
ccc agc cct gag cgg ttc ttc atg ccc ctg tac aag ggc tgc agc gga			926
Pro Ser Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly			
275	280	285	
gac ttc aag aaa tgg gtg ggt gca ccc ttc act ggc tcc agc ctg gag			974
Asp Phe Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu			
290	295	300	
ctg gga ccc tgg agc cca gag gtg ccc tcc acc ctg gag gtg tac agc			1022
Leu Gly Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser			
305	310	315	
tgc cac cca cca cgg agc ccg gcc aag agg ctg cag ctc acg gag cta			1070
Cys His Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu			
320	325	330	
caa gaa cca gca gag ctg gtg gag tct gac ggt gtg ccc aag ccc agc			1118
Gln Glu Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser			
335	340	345	350
ttc tgg ccg aca gcc cag aac tcg ggg ggc tca gct tac agt gag gag			1166
Phe Trp Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu			
355	360	365	

agg gat cgg cca tac ggc ctg gtg tcc att gac aca gtg act gtg cta	1214
Arg Asp Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu	
370 375 380	
gat gca gag ggg cca tgc acc tgg ccc tgc agc tgt gag gat gac ggc	1262
Asp Ala Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly	
385 390 395	
tac cca gcc ctg gac ctg gat gct ggc ctg gag ccc agc cca ggc cta	1310
Tyr Pro Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu	
400 405 410	
gag gac cca ctc ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt	1358
Glu Asp Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys	
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Val Ser Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu	
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gac aga cta aag cca ccc ctt gca gat ggg gag gac tgg gct ggg gga	1454
Asp Arg Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly	
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Leu Pro Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala	
465 470 475	
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Gly Ser Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe	
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Val Gly Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro	
495 500 505 510	
ggg gac gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att	1646
Gly Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile	
515 520 525	
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Pro Pro Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser	

530

535

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gcctgggata	atgcccattg	tactccatgc	attcacctgc	cctgtgcatg	tctggactca	1992
cggagctcac	ccatgtgcac	aagtgtgcac	agtaaactgt	tttgtggcca	acagatgaca	2052
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gcgatgtcac	ccgtgtacgg	tacgcagccc	agagcagacc	ctcaataaac	gtcagcttcc	2472
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aaatcagtcc	gtttcgtctc	ttggaacag	ctccccacca	accaagattt	ctttttctaa	2652
cttctgctac	taagttttta	aaaattccct	ttatgcaccc	aagagatatt	tattaaacac	2712
caattacgta	gcaggccatg	gctcatggga	cccaccccc	gtggcactca	tggagggggc	2772
tgcaggttgg	aactatgcag	tgtgctccgg	ccacacatcc	tgctggggcc	cctaccctgc	2832
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<213> Homo sapiens

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			20					25					30	
Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu
		35					40					45		
Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr
	50					55					60			
Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr
65					70				75					80
Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser
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Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser
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 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
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 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
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 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
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 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
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 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
 195 200 205
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
 225 230 235 240
 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
 245 250 255
 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
 260 265 270
 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
 275 280 285
 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
 290 295 300
 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
 305 310 315 320
 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
 325 330 335
 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
 340 345 350
 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
 355 360 365
 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
 370 375 380
 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
 385 390 395 400
 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
 405 410 415
 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
 420 425 430
 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
 435 440 445
 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro

450		455		460
Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser				
465		470		480
Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly				
	485		490	495
Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp				
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Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro				
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 <223> Xaa = Any Amino Acid

<221> VARIANT
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aayytncayc	cnwsnacnyt	nacnytnacn	tggcargayc	artaygarga	rytnaargay	180
gargcnacnw	sntgywsnyt	ncaymgwnsn	gcncayaayg	cnacncaygc	nacntayacn	240
tgycayatgg	aygtnttyca	yttatggcn	gaygayatht	tywsngtnaa	yathacngay	300
carwsnggna	aytaywsnca	rgartgyggn	wsnttyytny	tngcngarws	nathaarccn	360
gcncncnt	tyaaygtnac	ngtnacntty	wsnggncart	ayaayathws	ntggmgwnsn	420
gaytaygarg	ayccngcntt	ytayatgytn	aarggnaary	tncartayga	rytncartay	480
mgnaaymgng	gngayccntg	ggcngtnwsn	ccnmgmngna	arytnathws	ngtngaywsn	540
mgnwsngtnw	snytnytncc	nytngartty	mgnaargayw	snwsntayga	rytncargtn	600
mgngcnggnc	cnatgccngg	nwsnwsntay	carggnacnt	ggwsngartg	gwsngayccn	660
gtnathttyc	aracncarws	ngargarytn	aargarggnt	ggaayccnca	yytnytnytn	720
ytnytnytny	tngtnathgt	nttyathccn	gcnttytgww	snytnaarac	ncayccnytn	780
tgmgnytn	ggaaraarat	htgggcngtn	ccnwsnccng	armgnttytt	yatgccnytn	840
tayaarggnt	gywsnggnga	yttyaaraar	tgggtnggng	cncnttyac	nggnwsnwsn	900
ytngarytng	gnccntggws	nccngargtn	ccnwsnacny	tngargtnta	ywsntgyca	960
ccncnmgnw	sncngcnaa	rmgnytncar	ytnacngary	tncargarcc	ngcngarytn	1020
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gcnytngayy	tngaygcngg	nytngarccn	wsnccnggny	tngargaycc	nytnytngay	1260
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ccnytnngnw	snytnytnga	ymgnytnaar	ccncnytn	cngayggnga	rgaytgngcn	1380
ggnggnytn	cntggggngg	nmgnwsnccn	ggnggngtnw	sngarwsnga	rgcnggnwsn	1440
ccnytnngcng	gnytngayat	ggayacntty	gaywsnggnt	tygtnggnws	ngaytgywsn	1500
wsnccngtng	artgygaytt	yacnwsnccn	ggngaygarg	gnccnccnmg	nwsntayytn	1560
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 <212> DNA
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<220>
 <223> Oligonucleotide promoter ZC19931

<400> 42
 gggttggtacc gcaagatgcc gcgtggctgg gccgcc 36

<210> 43
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC19932

<400> 43
 cggaggatcc gtgagggttc cagccttcc 29

<210> 44
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer spanning vector flanking
 region and the 5' end of the zalphall

<400> 44

tccactttgc ctttctctcc acaggtgtcc agggaattca tcgataatgc cgcgtggctg	60
ggccgc	66

<210> 45

<211> 699

<212> DNA

<213> Homo sapiens

<400> 45

gagcccagat cttcagacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgag	60
ggggcaccgt cagtcttctt cttcccccca aaaccaagg acaccctcat gatctcccg	120
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc	360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccg	420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	540
cccgtgctgg actccgacgg ctctttcttc ctctacagca agctcaccgt ggacaagagc	600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	660
tacacgcaga agagcctctc cctgtctccg ggtaaataa	699

<210> 46

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> First Oligonucleotide primer spanning 3' end of the zalp11 extracellular domain and the 5' end of Fc4

<400> 46

gcacggtggg catgtgtgag ttttgtctga agatctgggc tcgtgagggt tccagccttc	60
ct	62

<210> 47

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Second Oligonucleotide primer spanning 3' end of the zalpha1 extracellular domain and the 5' end of Fc4

<400> 47

agaccagtc agaggagta aaggaaggct ggaaccctca cgagcccaga tcttcagaca 60
a 61

<210> 48

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer spanning the 3' end of Fc4 and the vector flanking region

<400> 48

gtgggcctct ggggtgggta caaccccaga gctgttttaa tctagattat ttacccggag 60
acaggga 67

<210> 49

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG tag amino acid sequence

<400> 49

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 50

<211> 1821

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide encoding MBP-zalpha1 soluble receptor fusion

<221> CDS

<222> (1)...(1821)

<400> 50

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Met	Lys	Ile	Glu	Glu	Gly	Lys	Leu	Val	Ile	Trp	Ile	Asn	Gly	Asp	Lys	
1				5					10					15		

ggc	tat	aac	ggt	ctc	gct	gaa	gtc	ggt	aag	aaa	ttc	gag	aaa	gat	acc	96
Gly	Tyr	Asn	Gly	Leu	Ala	Glu	Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	
			20					25						30		

gga	att	aaa	gtc	acc	ggt	gag	cat	ccg	gat	aaa	ctg	gaa	gag	aaa	ttc	144
Gly	Ile	Lys	Val	Thr	Val	Glu	His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	
			35					40						45		

cca	cag	gtt	gcg	gca	act	ggc	gat	ggc	cct	gac	att	atc	ttc	tgg	gca	192
Pro	Gln	Val	Ala	Ala	Thr	Gly	Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	
			50					55						60		

cac	gac	cg	ttt	ggt	ggc	tac	gct	caa	tct	ggc	ctg	ttg	gct	gaa	atc	240
His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	
	65					70				75				80		

acc	ccg	gac	aaa	gcg	ttc	cag	gac	aag	ctg	tat	ccg	ttt	acc	tgg	gat	288
Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	
				85					90					95		

gcc	gta	cgt	tac	aac	ggc	aag	ctg	att	gct	tac	ccg	atc	gct	gtt	gaa	336
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	
			100					105					110			

gcg	tta	tcg	ctg	att	tat	aac	aaa	gat	ctg	ctg	ccg	aac	ccg	cca	aaa	384
Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	
			115					120					125			

acc	tgg	gaa	gag	atc	ccg	gcg	ctg	gat	aaa	gaa	ctg	aaa	gcg	aaa	ggt	432
Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	
	130						135					140				

aag	agc	gcg	ctg	atg	ttc	aac	ctg	caa	gaa	ccg	tac	ttc	acc	tgg	ccg	480
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	
145						150				155					160	

ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys 165 170 175	528
tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly 180 185 190	576
ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp 195 200 205	624
acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gcg Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala 210 215 220	672
atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc aaa Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys 225 230 235 240	720
gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser 245 250 255	768
aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro 260 265 270	816
aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp 275 280 285	864
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala 290 295 300	912
ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala 305 310 315 320	960
acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln	1008

325	330	335	
atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc			1056
Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala			
340	345	350	
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat			1104
Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn			
355	360	365	
tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt			1152
Ser Ser Ser His His His His His Ala Asn Ser Val Pro Leu Val			
370	375	380	
ccg cgt gga tcc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag			1200
Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln			
385	390	395	400
acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc			1248
Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu			
405	410	415	
acc ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc			1296
Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr			
420	425	430	
tcc tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac			1344
Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr			
435	440	445	
acc tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt			1392
Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser			
450	455	460	
gtc aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc			1440
Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser			
465	470	475	480
ttt ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act			1488
Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr			
485	490	495	
gtg acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa			1536

Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu	
500 505 510	
gac cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag	1584
Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln	
515 520 525	
tac agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg	1632
Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu	
530 535 540	
atc tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc	1680
Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg	
545 550 555 560	
aaa gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc	1728
Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly	
565 570 575	
tcc tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt	1776
Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe	
580 585 590	
cag acc cag tca gag gag tta aag gaa ggc tgg aac cct cac tag	1821
Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His *	
595 600 605	

<210> 51

<211> 606

<212> PRT

<213> Artificial Sequence

<400> 51

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Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr	
20 25 30	
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe	
35 40 45	
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala	
50 55 60	
His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile	

65				70				75				80			
Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp
				85				90				95			
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu
			100					105				110			
Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys
		115					120					125			
Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly
	130					135					140				
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro
145					150					155					160
Leu	Ile	Ala	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys
				165					170					175	
Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly
			180					185					190		
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp
	195					200						205			
Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala
	210					215					220				
Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys
225					230					235					240
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser
			245						250					255	
Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro
			260					265					270		
Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp
	275					280						285			
Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala
	290					295					300				
Leu	Lys	Ser	Tyr	Glu	Glu	Glu	Leu	Ala	Lys	Asp	Pro	Arg	Ile	Ala	Ala
305					310					315					320
Thr	Met	Glu	Asn	Ala	Gln	Lys	Gly	Glu	Ile	Met	Pro	Asn	Ile	Pro	Gln
				325					330					335	
Met	Ser	Ala	Phe	Trp	Tyr	Ala	Val	Arg	Thr	Ala	Val	Ile	Asn	Ala	Ala
		340						345					350		
Ser	Gly	Arg	Gln	Thr	Val	Asp	Glu	Ala	Leu	Lys	Asp	Ala	Gln	Thr	Asn
	355					360						365			
Ser	Ser	Ser	His	His	His	His	His	His	Ala	Asn	Ser	Val	Pro	Leu	Val
	370				375					380					
Pro	Arg	Gly	Ser	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln
385					390					395					400
Thr	Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu
				405					410					415	

Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr
 420 425 430
 Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr
 435 440 445

 Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser
 450 455 460
 Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser
 465 470 475 480
 Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr
 485 490 495
 Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu
 500 505 510
 Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln
 515 520 525
 Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu
 530 535 540
 Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg
 545 550 555 560
 Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly
 565 570 575
 Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe
 580 585 590
 Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His
 595 600 605

<210> 52

<211> 657

<212> DNA

<213> Homo sapiens

<400> 52

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tggaacctcc	accccagcac	gctcaccctt	acctggcaag	accagtatga	agagctgaag	120
gacgaggcca	cctcctgcag	cctccacagg	tcggcccaca	atgccacgca	tgccacctac	180
acctgccaca	tggaatgtatt	ccacttcatg	gccgacgaca	ttttcagtgt	caacatcaca	240
gaccagtctg	gcaactactc	ccaggagtgt	ggcagctttc	tcctggctga	gagcatcaag	300
ccggctcccc	ctttcaacgt	gactgtgacc	ttctcaggac	agtataatat	ctcctggcgc	360
tcagattacg	aagaccctgc	cttctacatg	ctgaagggca	agcttcagta	tgagctgcag	420
tacaggaacc	ggggagaccc	ctgggctgtg	agtccgagga	gaaagctgat	ctcagtggac	480
tcaagaagtg	tctccctcct	ccccctggag	ttccgcaaag	actcgagcta	tgagctgcag	540
gtgcgggcag	ggcccatgcc	tggtcctcc	taccagggga	cctggagtga	atggagtgc	600
ccggtcatct	ttcagaccca	gtcagaggag	ttaaaggaag	gctggaaccc	tcactag	657

<210> 53
 <211> 65
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC20187

<400> 53
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 caccg 65

<210> 54
 <211> 68
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC20185

<400> 54
 tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ctagtgaggg ttccagcctt 60
 cctttaac 68

<210> 55
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC19372

<400> 55
 tgtcgatgaa gccctgaaag acgcgagac taattcgagc 40

<210> 56
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC19351

<400> 56
 acgcgcagac taattcgagc tcccaccatc accatcacca cgcgaattcg gtaccgctgg 60

<210> 57
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC19352

<400> 57
 actcactata gggcgaattg cccgggggat ccacgcggaa ccagcggtac cgaattcgcg 60

<210> 58
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC19371

<400> 58
 acggccagtg aattgtaata cgactcacta tagggcgaat tg 42

<210> 59
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC22277

<400> 59
 ccaggagtgt ggcagctttc 20

<210> 60
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC22276

<400> 60

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21

<210> 61

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> zalpha11 TaqMan probe, ZG31

<400> 61

cggctcccc tttcaacgtg act

23

<210> 62

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC23684

<400> 62

tcacccttac ctggcaagac

20

<210> 63

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC23656

<400> 63

taatacgact cactataggg agggggagac acttcttgag t

41

<210> 64

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC23685

<400> 64

aggtctgaat cccgactctg

20

<210> 65

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC23657

<400> 65

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41

<210> 66

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer, rRNA forward primer

<400> 66

cggctaccac atccaaggaa

20

<210> 67

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer, rRNA reverse primer

<400> 67

gctggaatta _ccgcggct

18

<210> 68

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> rRNA TaqMan probe

<400> 68

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22

<210> 69

<211> 1298

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (543)...(1262)

<400> 69

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aactagagac atccggaagt gtcaggagac ggagtagagg ctgggccact tagacctcag	180
gctctccctg cacacgtcct caagacctta ggacttagga acctggtccc agcaccagc	240
tgttccttgg ctggggcact ggtaactagc gtggatatga gacagaggac agtcagtcct	300
tactaaagggt gggaacacgg gctctgagaa cggacagtat tgggaacca ctgggcaggg	360
ggttcacaga cagacatcat ggcgcgtct ctctctctct ctctctcctg ttttcttggt	420
cttctgcttt ccccgctctt ggcttggtccc tgtactcccc cccccacccc catctttggc	480
tctctctggt cacacccgac ctgttggtcc ccagctcatg actgtgtggt tctttctcat	540
ag aaa tgg gtt aat acc cct ttc acg gcc tcc agc ata gag ttg gtg	587
Lys Trp Val Asn Thr Pro Phe Thr Ala Ser Ser Ile Glu Leu Val	
1 5 10 15	

cca cag agt tcc aca aca aca tca gcc tta cat ctg tca ttg tat cca	635
Pro Gln Ser Ser Thr Thr Thr Ser Ala Leu His Leu Ser Leu Tyr Pro	
20 25 30	

gcc aag gag aag aag ttc ccg ggg ctg ccg ggt ctg gaa gag caa ctg	683
Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro Gly Leu Glu Glu Gln Leu	
35 40 45	

gag tgt gat gga atg tct gag cct ggt cac tgg tgc ata atc ccc ttg	731
Glu Cys Asp Gly Met Ser Glu Pro Gly His Trp Cys Ile Ile Pro Leu	
50 55 60	

gca gct ggc caa gcg gtc tca gcc tac agt gag gag aga gac cgg cca	779
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Ala	Ala	Gly	Gln	Ala	Val	Ser	Ala	Tyr	Ser	Glu	Glu	Arg	Asp	Arg	Pro	
65						70					75					
tat	ggg	ctg	gtg	tcc	att	gac	aca	gtg	act	gtg	gga	gat	gca	gag	ggc	827
Tyr	Gly	Leu	Val	Ser	Ile	Asp	Thr	Val	Thr	Val	Gly	Asp	Ala	Glu	Gly	
80					85					90					95	
ctg	tgt	gtc	tgg	ccc	tgt	agc	tgt	gag	gat	gat	ggc	tat	cca	gcc	atg	875
Leu	Cys	Val	Trp	Pro	Cys	Ser	Cys	Glu	Asp	Asp	Gly	Tyr	Pro	Ala	Met	
				100					105					110		
aac	ctg	gat	gct	ggc	cga	gag	tct	ggc	cct	aat	tca	gag	gat	ctg	ctc	923
Asn	Leu	Asp	Ala	Gly	Arg	Glu	Ser	Gly	Pro	Asn	Ser	Glu	Asp	Leu	Leu	
			115					120					125			
ttg	gtc	aca	gac	cct	gct	ttt	ctg	tct	tgc	ggc	tgt	gtc	tca	ggg	agt	971
Leu	Val	Thr	Asp	Pro	Ala	Phe	Leu	Ser	Cys	Gly	Cys	Val	Ser	Gly	Ser	
		130					135					140				
ggg	ctc	agg	ctt	gga	ggc	tcc	cca	ggc	agc	cta	ctg	gac	agg	ttg	agg	1019
Gly	Leu	Arg	Leu	Gly	Gly	Ser	Pro	Gly	Ser	Leu	Leu	Asp	Arg	Leu	Arg	
145						150					155					
ctg	tca	ttt	gca	aag	gaa	ggg	gac	tgg	aca	gca	gac	cca	acc	tgg	aga	1067
Leu	Ser	Phe	Ala	Lys	Glu	Gly	Asp	Trp	Thr	Ala	Asp	Pro	Thr	Trp	Arg	
160					165					170					175	
act	ggg	tcc	cca	gga	ggg	ggc	tct	gag	agt	gaa	gca	ggg	tcc	ccc	cct	1115
Thr	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Glu	Ser	Glu	Ala	Gly	Ser	Pro	Pro	
				180					185					190		
ggg	ctg	gac	atg	gac	aca	ttt	gac	agt	ggc	ttt	gca	ggg	tca	gac	tgt	1163
Gly	Leu	Asp	Met	Asp	Thr	Phe	Asp	Ser	Gly	Phe	Ala	Gly	Ser	Asp	Cys	
			195					200					205			
ggc	agc	ccc	gtg	gag	act	gat	gaa	gga	ccc	cct	cga	agc	tat	ctc	cgc	1211
Gly	Ser	Pro	Val	Glu	Thr	Asp	Glu	Gly	Pro	Pro	Arg	Ser	Tyr	Leu	Arg	
		210					215					220				
cag	tgg	gtg	gtc	agg	acc	cct	cca	cct	gtg	gac	agt	gga	gcc	cag	agc	1259
Gln	Trp	Val	Val	Arg	Thr	Pro	Pro	Pro	Val	Asp	Ser	Gly	Ala	Gln	Ser	
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1298

Ser

240

<210> 70

<211> 240

<212> PRT

<213> Mus musculus

<400> 70

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Gln	Ser	Ser	Thr	Thr	Thr	Ser	Ala	Leu	His	Leu	Ser	Leu	Tyr	Pro	Ala
			20				25						30		
Lys	Glu	Lys	Lys	Phe	Pro	Gly	Leu	Pro	Gly	Leu	Glu	Glu	Gln	Leu	Glu
	35					40					45				
Cys	Asp	Gly	Met	Ser	Glu	Pro	Gly	His	Trp	Cys	Ile	Ile	Pro	Leu	Ala
50					55			60							
Ala	Gly	Gln	Ala	Val	Ser	Ala	Tyr	Ser	Glu	Glu	Arg	Asp	Arg	Pro	Tyr
65				70				75						80	
Gly	Leu	Val	Ser	Ile	Asp	Thr	Val	Thr	Val	Gly	Asp	Ala	Glu	Gly	Leu
			85			90							95		
Cys	Val	Trp	Pro	Cys	Ser	Cys	Glu	Asp	Asp	Gly	Tyr	Pro	Ala	Met	Asn
		100				105						110			
Leu	Asp	Ala	Gly	Arg	Glu	Ser	Gly	Pro	Asn	Ser	Glu	Asp	Leu	Leu	Leu
	115				120						125				
Val	Thr	Asp	Pro	Ala	Phe	Leu	Ser	Cys	Gly	Cys	Val	Ser	Gly	Ser	Gly
	130				135						140				
Leu	Arg	Leu	Gly	Gly	Ser	Pro	Gly	Ser	Leu	Leu	Asp	Arg	Leu	Arg	Leu
145				150				155						160	
Ser	Phe	Ala	Lys	Glu	Gly	Asp	Trp	Thr	Ala	Asp	Pro	Thr	Trp	Arg	Thr
			165			170							175		
Gly	Ser	Pro	Gly	Gly	Gly	Ser	Glu	Ser	Glu	Ala	Gly	Ser	Pro	Pro	Gly
		180			185								190		
Leu	Asp	Met	Asp	Thr	Phe	Asp	Ser	Gly	Phe	Ala	Gly	Ser	Asp	Cys	Gly
	195				200						205				
Ser	Pro	Val	Glu	Thr	Asp	Glu	Gly	Pro	Pro	Arg	Ser	Tyr	Leu	Arg	Gln
	210				215						220				
Trp	Val	Val	Arg	Thr	Pro	Pro	Pro	Val	Asp	Ser	Gly	Ala	Gln	Ser	Ser
225				230					235					240	

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<400> 71
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<210> 72
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<220>
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<400> 72
 tctgaacctg caaagccact gtc 23

<210> 73
 <211> 27
 <212> DNA
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<220>
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<400> 73
 ccatcctaatac gactcact atagggc 27

<210> 74
 <211> 22
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<220>
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<400> 74
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<210> 75
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<400> 75
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<210> 76
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<400> 76
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<210> 77
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 <212> DNA
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<220>
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<400> 77
 tccagcatag agttggtgcc aca 23

<210> 78
 <211> 592
 <212> DNA
 <213> Mus musculus

<220>
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 <222> (436)...(592)

<400> 78

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gggcagccaa ctggcctcag cccgtgcccc aggcgtgccc tgtctctgtc tggtgcccc    180
agccctactg tcttcctctg tgtaggctct gccagatgc ccggctggtc ctcagcctca    240
ggactatctc agcagtgact cccctgattc tggacttgca cctgactgaa ctcctgccc    300
cctcaaacct tcacctcca ccaccaccac tccgagtccc gctgtgactc ccacgcccag    360
gagaccaccc aagtgcccc gcctaaagaa tggctttctg aggaagatcc tgaaggagta    420
ggtctgggac acagc atg ccc cgg ggc cca gtg gct gcc tta ctc ctg ctg    471

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Met Pro Arg Gly Pro Val Ala Ala Leu Leu Leu Leu

1

5

10

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att ctc cat gga gct tgg agc tgc ctg grc ctc act tgc tac act gac    519
Ile Leu His Gly Ala Trp Ser Cys Leu Xaa Leu Thr Cys Tyr Thr Asp
      15                20                25

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tac ctc tgg acc atc acc tgt gtc ctg gag aca cgg agc ccc aac ccc    567
Tyr Leu Trp Thr Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro
      30                35                40

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agc ata ctc agt ctc acc tgg caa g    592
Ser Ile Leu Ser Leu Thr Trp Gln
      45                50

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<210> 79

<211> 52

<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> (1)...(51)

<223> Xaa = Any Amino Acid

<400> 79

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Ala Trp Ser Cys Leu Xaa Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr
      20                25                30
Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser
      35                40                45
Leu Thr Trp Gln
      50

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 <212> DNA
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<220>
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<400> 80

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Arg Tyr Asp Ile Ser Trp Asp Ser Ala Tyr Asp Glu Pro Ser Asn	
1 5 10 15	

tac gtg ctg aga ggc aag cta caa tat gag ctg cag tat cgg aac ctc	95
Tyr Val Leu Arg Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Leu	
20 25 30	

aga gac ccc tat gct gtg agg ccg gtg acc aag ctg atc tca gtg gac	143
Arg Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile Ser Val Asp	
35 40 45	

tca aga aac gtc tct ctt ctc cct gaa gag ttc cac aaa gat tct agc	191
Ser Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys Asp Ser Ser	
50 55 60	

tac cag ctg cag atg cgg gca gcg cct cag cca ggc act tca ttc agg	239
Tyr Gln Leu Gln Met Arg Ala Ala Pro Gln Pro Gly Thr Ser Phe Arg	
65 70 75	

ggg acc tgg agt gag tgg agt gac ccc gtc atc ttt cgg acc cag gct	287
Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Arg Thr Gln Ala	
80 85 90 95	

ggg gag ccc gag gca ggc tgg gac cct cac atg ctg ctg ctc ctg gct	335
Gly Glu Pro Glu Ala Gly Trp Asp Pro His Met Leu Leu Leu Leu Ala	
100 105 110	

gtc ttg atc att gtc ctg gtt ttc atg ggt ctg aag atc cac ctg cct	383
Val Leu Ile Ile Val Leu Val Phe Met Gly Leu Lys Ile His Leu Pro	
115 120 125	

tgg agg cta tgg aaa aag ata tgg gca cca gtg ccc acc cct gag agt	431
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Trp	Arg	Leu	Trp	Lys	Lys	Ile	Trp	Ala	Pro	Val	Pro	Thr	Pro	Glu	Ser	
		130					135					140				
ttc	ttc	cag	ccc	ctg	tgc	agg	gag	cac	agc	ggg	aac	ttc	aag	aaa	tgg	479
Phe	Phe	Gln	Pro	Leu	Cys	Arg	Glu	His	Ser	Gly	Asn	Phe	Lys	Lys	Trp	
		145				150					155					
gtt	aat	acc	cct	ttc	acg	gcc	tcc	agc	ata	gag	ttg	gtg	cca	cag	agt	527
Val	Asn	Thr	Pro	Phe	Thr	Ala	Ser	Ser	Ile	Glu	Leu	Val	Pro	Gln	Ser	
160					165					170					175	
tcc	aca	aca	aca	tca	gcc	tta	cat	ctg	tca	ttg	tat	cca	gcc	aag	gag	575
Ser	Thr	Thr	Thr	Ser	Ala	Leu	His	Leu	Ser	Leu	Tyr	Pro	Ala	Lys	Glu	
				180					185					190		
aag	aag	ttc	ccg	ggg	ctg	ccg	ggt	ctg	gaa	gag	caa	ctg	gag	tgt	gat	623
Lys	Lys	Phe	Pro	Gly	Leu	Pro	Gly	Leu	Glu	Glu	Gln	Leu	Glu	Cys	Asp	
			195				200					205				
gga	atg	tct	gag	cct	ggt	cac	tgg	tgc	ata	atc	ccc	ttg	gca	gct	ggc	671
Gly	Met	Ser	Glu	Pro	Gly	His	Trp	Cys	Ile	Ile	Pro	Leu	Ala	Ala	Gly	
	210						215					220				
caa	gcg	gtc	tca	gcc	tac	agt	gag	gag	aga	gac	cgg	cca	tat	ggt	ctg	719
Gln	Ala	Val	Ser	Ala	Tyr	Ser	Glu	Glu	Arg	Asp	Arg	Pro	Tyr	Gly	Leu	
	225					230					235					
gtg	tcc	att	gac	aca	gtg	act	gtg	gga	gat	gca	gag	ggc	ctg	tgt	gtc	767
Val	Ser	Ile	Asp	Thr	Val	Thr	Val	Gly	Asp	Ala	Glu	Gly	Leu	Cys	Val	
240					245					250					255	
tgg	ccc	tgt	agc	tgt	gag	gat	gat	ggc	tat	cca	gcc	atg	aac	ctg	gat	815
Trp	Pro	Cys	Ser	Cys	Glu	Asp	Asp	Gly	Tyr	Pro	Ala	Met	Asn	Leu	Asp	
				260					265					270		
gct	ggc	cga	gag	tct	ggc	cct	aat	tca	gag	gat	ctg	ctc	ttg	gtc	aca	863
Ala	Gly	Arg	Glu	Ser	Gly	Pro	Asn	Ser	Glu	Asp	Leu	Leu	Leu	Val	Thr	
			275					280					285			
gac	cct	gct	ttt	ctg	tct	tgc	ggc	tgt	gtc	tca	ggt	agt	ggt	ctc	agg	911
Asp	Pro	Ala	Phe	Leu	Ser	Cys	Gly	Cys	Val	Ser	Gly	Ser	Gly	Leu	Arg	
		290					295					300				

ctt gga ggc tcc cca ggc agc cta ctg gac agg ttg agg ctg tca ttt 959
 Leu Gly Gly Ser Pro Gly Ser Leu Leu Asp Arg Leu Arg Leu Ser Phe
 305 310 315

gca aag gaa ggg gac tgg aca gca gac cca acc tgg aga act ggg tcc 1007
 Ala Lys Glu Gly Asp Trp Thr Ala Asp Pro Thr Trp Arg Thr Gly Ser
 320 325 330 335

cca gga ggg ggc tct gag agt gaa gca ggt tcc ccc cct ggt ctg gac 1055
 Pro Gly Gly Gly Ser Glu Ser Glu Ala Gly Ser Pro Pro Gly Leu Asp
 340 345 350

atg gac aca ttt gac agt ggc ttt gca ggt tca gac tgt ggc agc ccc 1103
 Met Asp Thr Phe Asp Ser Gly Phe Ala Gly Ser Asp Cys Gly Ser Pro
 355 360 365

gtg gag act gat gaa gga ccc cct cga agc tat ctc cgc cag tgg gtg 1151
 Val Glu Thr Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val
 370 375 380

gtc agg acc cct cca cct gtg gac agt gga gcc cag agc agc tag 1196
 Val Arg Thr Pro Pro Pro Val Asp Ser Gly Ala Gln Ser Ser *
 385 390 395

catataataa ccagctatag tgagaagagg cct 1229

<210> 81

<211> 397

<212> PRT

<213> Mus musculus

<400> 81

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 20 25 30
 Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile Ser Val Asp Ser
 35 40 45
 Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys Asp Ser Ser Tyr
 50 55 60
 Gln Leu Gln Met Arg Ala Ala Pro Gln Pro Gly Thr Ser Phe Arg Gly
 65 70 75 80

Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Arg Thr Gln Ala Gly
 85 90 95
 Glu Pro Glu Ala Gly Trp Asp Pro His Met Leu Leu Leu Leu Ala Val
 100 105 110
 Leu Ile Ile Val Leu Val Phe Met Gly Leu Lys Ile His Leu Pro Trp
 115 120 125
 Arg Leu Trp Lys Lys Ile Trp Ala Pro Val Pro Thr Pro Glu Ser Phe
 130 135 140
 Phe Gln Pro Leu Cys Arg Glu His Ser Gly Asn Phe Lys Lys Trp Val
 145 150 155 160
 Asn Thr Pro Phe Thr Ala Ser Ser Ile Glu Leu Val Pro Gln Ser Ser
 165 170 175
 Thr Thr Thr Ser Ala Leu His Leu Ser Leu Tyr Pro Ala Lys Glu Lys
 180 185 190
 Lys Phe Pro Gly Leu Pro Gly Leu Glu Glu Gln Leu Glu Cys Asp Gly
 195 200 205
 Met Ser Glu Pro Gly His Trp Cys Ile Ile Pro Leu Ala Ala Gly Gln
 210 215 220
 Ala Val Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro Tyr Gly Leu Val
 225 230 235 240
 Ser Ile Asp Thr Val Thr Val Gly Asp Ala Glu Gly Leu Cys Val Trp
 245 250 255
 Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Met Asn Leu Asp Ala
 260 265 270
 Gly Arg Glu Ser Gly Pro Asn Ser Glu Asp Leu Leu Leu Val Thr Asp
 275 280 285
 Pro Ala Phe Leu Ser Cys Gly Cys Val Ser Gly Ser Gly Leu Arg Leu
 290 295 300
 Gly Gly Ser Pro Gly Ser Leu Leu Asp Arg Leu Arg Leu Ser Phe Ala
 305 310 315 320
 Lys Glu Gly Asp Trp Thr Ala Asp Pro Thr Trp Arg Thr Gly Ser Pro
 325 330 335

 Gly Gly Gly Ser Glu Ser Glu Ala Gly Ser Pro Pro Gly Leu Asp Met
 340 345 350
 Asp Thr Phe Asp Ser Gly Phe Ala Gly Ser Asp Cys Gly Ser Pro Val
 355 360 365
 Glu Thr Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val
 370 375 380
 Arg Thr Pro Pro Pro Val Asp Ser Gly Ala Gln Ser Ser
 385 390 395

<211> 23
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<220>
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<400> 82
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<210> 83
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 83
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<210> 84
 <211> 1735
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (143)...(1729)

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 cgcccaggag accacccaag tgcccagcc taaagaatgg ctttctgaga aagaccctga 120
 aggagtaggt ctgggacaca gc atg ccc cgg ggc cca gtg gct gcc tta ctc 172

Met Pro Arg Gly Pro Val Ala Ala Leu Leu
 1 5 10

ctg ctg att ctc cat gga gct tgg agc tgc ctg gac ctc act tgc tac 220
 Leu Leu Ile Leu His Gly Ala Trp Ser Cys Leu Asp Leu Thr Cys Tyr
 15 20 25

act gac tac ctc tgg acc atc acc tgt gtc ctg gag aca cgg agc ccc 268

Thr	Asp	Tyr	Leu	Trp	Thr	Ile	Thr	Cys	Val	Leu	Glu	Thr	Arg	Ser	Pro	
			30					35					40			
aac	ccc	agc	ata	ctc	agt	ctc	acc	tgg	caa	gat	gaa	tat	gag	gaa	ctt	316
Asn	Pro	Ser	Ile	Leu	Ser	Leu	Thr	Trp	Gln	Asp	Glu	Tyr	Glu	Glu	Leu	
		45					50				55					
cag	gac	caa	gag	acc	ttc	tgc	agc	cta	cac	agg	tct	ggc	cac	aac	acc	364
Gln	Asp	Gln	Glu	Thr	Phe	Cys	Ser	Leu	His	Arg	Ser	Gly	His	Asn	Thr	
	60					65				70						
aca	cat	ata	tgg	tac	acg	tgc	cat	atg	cgc	ttg	tct	caa	ttc	ctg	tcc	412
Thr	His	Ile	Trp	Tyr	Thr	Cys	His	Met	Arg	Leu	Ser	Gln	Phe	Leu	Ser	
75					80					85					90	
gat	gaa	gtt	ttc	att	gtc	aat	gtg	acg	gac	cag	tct	ggc	aac	aac	tcc	460
Asp	Glu	Val	Phe	Ile	Val	Asn	Val	Thr	Asp	Gln	Ser	Gly	Asn	Asn	Ser	
				95				100						105		
caa	gag	tgt	ggc	agc	ttt	gtc	ctg	gct	gag	agc	atc	aaa	cca	gct	ccc	508
Gln	Glu	Cys	Gly	Ser	Phe	Val	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	
			110					115					120			
ccc	ttg	aac	gtg	act	gtg	gcc	ttc	tca	gga	cgc	tat	gat	atc	tcc	tgg	556
Pro	Leu	Asn	Val	Thr	Val	Ala	Phe	Ser	Gly	Arg	Tyr	Asp	Ile	Ser	Trp	
		125					130					135				
gac	tca	gct	tat	gac	gaa	ccc	tcc	aac	tac	gtg	ctg	agg	ggc	aag	cta	604
Asp	Ser	Ala	Tyr	Asp	Glu	Pro	Ser	Asn	Tyr	Val	Leu	Arg	Gly	Lys	Leu	
	140					145					150					
caa	tat	gag	ctg	cag	tat	cgg	aac	ctc	aga	gac	ccc	tat	gct	gtg	agg	652
Gln	Tyr	Glu	Leu	Gln	Tyr	Arg	Asn	Leu	Arg	Asp	Pro	Tyr	Ala	Val	Arg	
155					160					165					170	
ccg	gtg	acc	aag	ctg	atc	tca	gtg	gac	tca	aga	aac	gtc	tct	ctt	ctc	700
Pro	Val	Thr	Lys	Leu	Ile	Ser	Val	Asp	Ser	Arg	Asn	Val	Ser	Leu	Leu	
				175				180						185		
cct	gaa	gag	ttc	cac	aaa	gat	tct	agc	tac	cag	ctg	cag	gtg	cgg	gca	748
Pro	Glu	Glu	Phe	His	Lys	Asp	Ser	Ser	Tyr	Gln	Leu	Gln	Val	Arg	Ala	
			190					195					200			

gcg cct cag cca ggc act tca ttc agg ggg acc tgg agt gag tgg agt	796
Ala Pro Gln Pro Gly Thr Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser	
205 210 215	
gac ccc gtc atc ttt cag acc cag gct ggg gag ccc gag gca ggc tgg	844
Asp Pro Val Ile Phe Gln Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp	
220 225 230	
gac cct cac atg ctg ctg ctc ctg gct gtc ttg atc att gtc ctg gtt	892
Asp Pro His Met Leu Leu Leu Leu Ala Val Leu Ile Ile Val Leu Val	
235 240 245 250	
ttc atg ggt ctg aag atc cac ctg cct tgg agg cta tgg aaa aag ata	940
Phe Met Gly Leu Lys Ile His Leu Pro Trp Arg Leu Trp Lys Lys Ile	
255 260 265	
tgg gca cca gtg ccc acc cct gag agt ttc ttc cag ccc ctg tac agg	988
Trp Ala Pro Val Pro Thr Pro Glu Ser Phe Phe Gln Pro Leu Tyr Arg	
270 275 280	
gag cac agc ggg aac ttc aag aaa tgg gtt aat acc cct ttc acg gcc	1036
Glu His Ser Gly Asn Phe Lys Lys Trp Val Asn Thr Pro Phe Thr Ala	
285 290 295	
tcc agc ata gag ttg gtg cca cag agt tcc aca aca aca tca gcc tta	1084
Ser Ser Ile Glu Leu Val Pro Gln Ser Ser Thr Thr Thr Ser Ala Leu	
300 305 310	
cat ctg tca ttg tat cca gcc aag gag aag aag ttc ccg ggg ctg ccg	1132
His Leu Ser Leu Tyr Pro Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro	
315 320 325 330	
ggt ctg gaa gag caa ctg gag tgt gat gga atg tct gag cct ggt cac	1180
Gly Leu Glu Glu Gln Leu Glu Cys Asp Gly Met Ser Glu Pro Gly His	
335 340 345	
tgg tgc ata atc ccc ttg gca gct ggc caa gcg gtc tca gcc tac agt	1228
Trp Cys Ile Ile Pro Leu Ala Ala Gly Gln Ala Val Ser Ala Tyr Ser	
350 355 360	
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 <211> 529
 <212> PRT
 <213> Mus musculus

<400> 85
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 Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser
 35 40 45
 Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe
 50 55 60
 Cys Ser Leu His Arg Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr
 65 70 75 80
 Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val
 85 90 95
 Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe
 100 105 110
 Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val
 115 120 125
 Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp Asp Ser Ala Tyr Asp Glu
 130 135 140
 Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160
 Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys
 180 185 190
 Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala Ala Pro Gln Pro Gly Thr
 195 200 205
 Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp Asp Pro His Met Leu Leu
 225 230 235 240
 Leu Leu Ala Val Leu Ile Ile Val Leu Val Phe Met Gly Leu Lys Ile
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 His Leu Pro Trp Arg Leu Trp Lys Lys Ile Trp Ala Pro Val Pro Thr
 260 265 270
 Pro Glu Ser Phe Phe Gln Pro Leu Tyr Arg Glu His Ser Gly Asn Phe
 275 280 285

Lys Lys Trp Val Asn Thr Pro Phe Thr Ala Ser Ser Ile Glu Leu Val
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 Pro Gln Ser Ser Thr Thr Thr Ser Ala Leu His Leu Ser Leu Tyr Pro
 305 310 315 320
 Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro Gly Leu Glu Glu Gln Leu
 325 330 335
 Glu Cys Asp Gly Met Ser Glu Pro Gly His Trp Cys Ile Ile Pro Leu
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 Ala Ala Gly Gln Ala Val Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro
 355 360 365
 Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Gly Asp Ala Glu Gly
 370 375 380
 Leu Cys Val Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Met
 385 390 395 400
 Asn Leu Asp Ala Gly Arg Glu Ser Gly Pro Asn Ser Glu Asp Leu Leu
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 Leu Val Thr Asp Pro Ala Phe Leu Ser Cys Gly Cys Val Ser Gly Ser
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 Gly Leu Arg Leu Gly Gly Ser Pro Gly Ser Leu Leu Asp Arg Leu Arg
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 Leu Ser Phe Ala Lys Glu Gly Asp Trp Thr Ala Asp Pro Thr Trp Arg
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 Thr Gly Ser Pro Gly Gly Gly Ser Glu Ser Glu Ala Gly Ser Pro Pro
 465 470 475 480
 Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Ala Gly Ser Asp Cys
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